=> d his

         FILE 'CAPLUS' ENTERED AT 14:38:59 ON 13 JAN 2004
    L1   226 S ?METHYMYCIN OR PIKROMYCIN OR PICROMYCIN OR NARBOMYCIN
    L2   41 S L1 AND (POLYKETIDE (2W) SYNTHASE)
    L3   37 S L1 (P) (POLYKETIDE (2W) SYNTHASE)
    L4   30 S L1 (S) (POLYKETIDE (2W) SYNTHASE)
    L5   14 S L4 AND VENEZUELAE
    L6   3 S L2 AND PROMOTER
    L7   44 S L1 AND GENE
    L8   29 S L7 AND POLYKETIDE
    L9   26 S L7 AND VENEZUELAE

    L6   ANSWER 1 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
    AN   2000:756845   CAPLUS
    TI   A method for preparing large libraries of polyketides and non-ribosomal
         peptides using combinations of plasmids carrying genes for different
         functional domains of the biosynthetic enzymes
    IN   Santi, Daniel V.; Xue, Qun; Ashley, Gary
    PA   Kosan Biosciences, Inc., USA
    SO   PCT Int. Appl., 32 pp.
         PATENT NO.   KIND DATE   APPLICATION NO.   DATE
         --------------- ---- --------   ---------------- --------
    PI   WO 2000063361   A2   20001026   WO 2000-US10021   20000412
         WO 2000063361   A3   20010712
         EP 1171583   A2   20020116   EP 2000-922192   20000412
         JP 2003504006   T2   20030204   JP 2000-612440   20000412
    PRAI US 1999-129731P P   19990416
         WO 2000-US10021 W   20000412

    L6   ANSWER 2 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
    AN   1999:764178   CAPLUS
    TI   Sequence and recombinant narbonolide polyketide synthase
         applications from Streptomyces venezuelae for creation of useful
         antibiotics
    IN   Ashley, Gary; Betlach, Melanie C.; Betlach, Mary; McDaniel, Robert; Tang,
         Li
    PA   Kosan Biosciences, Inc., USA
    SO   PCT Int. Appl., 98 pp.
         PATENT NO.   KIND DATE   APPLICATION NO.   DATE
         --------------- ---- --------   ---------------- --------
    PI   WO 9961599   A2   19991202   WO 1999-US11814   19990527
         WO 9961599   A3   20000127
         US 6503741   B1   20030107   US 1998-141908   19980828
         CA 2328427   AA   19991202   CA 1999-2328427   19990527
         AU 9942137   A1   19991213   AU 1999-42137   19990527
         AU 762399   B2   20030626
         EP 1082439   A2   20010314   EP 1999-925954   19990527
         JP 2002516090   T2   20020604   JP 2000-550984   19990527
         NZ 509006   A   20030926   NZ 1999-509006   19990527
    PRAI US 1998-87080P   P   19980528
         US 1998-141908   A   19980828
         US 1998-100880P P   19980922
         US 1999-119139P P   19990208
         WO 1999-US11814 W   19990527

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L6    ANSWER 3 OF 3  CAPLUS  COPYRIGHT 2004 ACS on STN
AN    1997:501482  CAPLUS
TI    Polyhydroxyalkanoate synthase recombinant production and novel pathway for
      polyhydroxyalkanoate synthesis
IN    Sherman, David H.; Williams, Mark D.; Xue, Yongquan
PA    Regents of the University of Minnesota, USA; Sherman, David H.; Williams,
      Mark D.; Xue, Yongquan
SO    PCT Int. Appl., 90 pp.
      PATENT NO.          KIND  DATE        APPLICATION NO.   DATE
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PI    WO 9722711          A1    19970626    WO 1996-US20119   19961218
      EP 870053           A1    19981014    EP 1996-944849    19961218
      JP 2000502256       T2    20000229    JP 1997-522970    19961218
      US 6600029          B1    20030729    US 1998-91609     19980619
PRAI  US 1995-8847P       P     19951219
      WO 1996-US20119     W     19961218


L9    ANSWER 2 OF 26  CAPLUS  COPYRIGHT 2004 ACS on STN
AN    2003:435232  CAPLUS
TI    Engineering of recombinant Streptomyces venezuelae narbonolide
      polyketide synthase for production of novel polyketide products
IN    Ashley, Gary; Betlach, Melanie C.; Betlach, Mary; McDaniel, Robert; Tang,
      Li
PA    USA
SO    U.S. Pat. Appl. Publ., 74 pp., Cont.-in-part of U. S. Ser. No. 657,440.
      PATENT NO.          KIND  DATE        APPLICATION NO.   DATE
      ---------------     ----  --------    ----------------  --------
PI    US 2003104597       A1    20030605    US 2001-793708    20010222
      US 2002034797       A1    20020321    US 1997-846247    19970430
      US 6391594          B2    20020521
      US 6558942          B1    20030506    US 1998-73538     19980506
      US 6503741          B1    20030107    US 1998-141908    19980828
      US 6117659          A     20000912    US 1999-320878    19990527
      US 6509455          B1    20030121    US 2000-657440    20000907
      WO 2002097062       A2    20021205    WO 2002-US5642    20020222
      US 2003162262       A1    20030828    US 2002-160539    20020529
PRAI  US 1997-846247      A2    19970430
      US 1998-73538       A2    19980506
      US 1998-87080P      P     19980528
      US 1998-141908      A2    19980828
      US 1998-100880P     P     19980922
      US 1999-119139P     P     19990208
      US 1999-134990P     P     19990520
      US 1999-320878      A     19990527
      US 2000-657440      A2    20000907
      US 1994-238811      A2    19940506
      US 1995-486645      A1    19950607
      US 1998-79919P      P     19980305
      US 2001-793708      A     20010222
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L9    ANSWER 4 OF 26  CAPLUS  COPYRIGHT 2004 ACS on STN
AN    2002:927567  CAPLUS
TI    Recombinant narbonolide polyketide synthase for the production of
      polyketides useful as antibiotics
IN    Ashley, Gary; Betlach, Melanie C.; Betlach, Mary; McDaniel, Robert; Tang,
      Li
PA    Kosan Biosciences, Inc., USA
SO    PCT Int. Appl., 127 pp.
      PATENT NO.        KIND  DATE          APPLICATION NO.   DATE
      ---------------   ----  --------      ---------------   --------
PI    WO 2002097062     A2    20021205      WO 2002-US5642    20020222
      US 2003104597     A1    20030605      US 2001-793708    20010222
PRAI  US 2001-793708    A     20010222
      US 1997-846247    A2    19970430
      US 1998-73538     A2    19980506
      US 1998-87080P    P     19980528
      US 1998-141908    A2    19980828
      US 1998-100880P   P     19980922
      US 1999-119139P   P     19990208
      US 1999-134990P   P     19990520
      US 1999-320878    A     19990527
      US 2000-657440    A2    20000907

L9    ANSWER 6 OF 26  CAPLUS  COPYRIGHT 2004 ACS on STN
AN    2002:276140  CAPLUS
TI    Recombinant bacteria producing substances with altered sugar moieties and
      their use for production of these substances
IN    Liu, Hung-Wen; Sherman, David H.; Zhao, Lishan
PA    Regents of the University of Minnesota, USA
SO    PCT Int. Appl., 174 pp.
      PATENT NO.        KIND  DATE          APPLICATION NO.   DATE
      ---------------   ----  --------      ---------------   --------
PI    WO 2002029035     A2    20020411      WO 2001-US31255   20011005
      WO 2002029035     A3    20030130
      AU 2001096652     A5    20020415      AU 2001-96652     20011005
      EP 1325134        A2    20030709      EP 2001-977540    20011005
PRAI  US 2000-238185P   P     20001005
      WO 2001-US31255   W     20011005

L9    ANSWER 8 OF 26  CAPLUS  COPYRIGHT 2004 ACS on STN
AN    2001:392662  CAPLUS
TI    Characterization and analysis of the PikD regulatory factor in the
      pikromycin biosynthetic pathway of Streptomyces venezuelae
AU    Wilson, Daniel J.; Xue, Yongquan; Reynolds, Kevin A.; Sherman, David H.
SO    Journal of Bacteriology (2001), 183(11), 3468-3475
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June
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L9    ANSWER 9 OF 26  CAPLUS  COPYRIGHT 2004 ACS on STN
AN    2001:127810  CAPLUS
TI    The Streptomyces venezuelae pikAV gene contains a
      transcription unit essential for expression of enzymes involved in
      glycosylation of narbonolide and 10-deoxymethynolide
AU    Chen, S.; Roberts, J. B.; Xue, Y.; Sherman, D. H.; Reynolds, K. A.
SO    Gene (2001), 263(1-2), 255-264
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Jan

```
L9     ANSWER 10 OF 26  CAPLUS  COPYRIGHT 2004 ACS on STN
AN     2001:79736  CAPLUS
TI     Biosynthesis and combinatorial biosynthesis of pikromycin
       -related macrolides in Streptomyces venezuelae
AU     Xue, Yongquan; Sherman, David H.
SO     Metabolic Engineering (2001), 3(1), 15-26
```

Jan

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L9     ANSWER 13 OF 26  CAPLUS  COPYRIGHT 2004 ACS on STN
AN     2000:152485  CAPLUS
TI     Genetic architecture of the polyketide synthases for methymycin
       and pikromycin series macrolides
AU     Xue, Y.; Wilson, D.; Sherman, D. H.
SO     Gene (2000), 245(1), 203-211


L9     ANSWER 14 OF 26  CAPLUS  COPYRIGHT 2004 ACS on STN
AN     2000:15381  CAPLUS
TI     Gene clusters encoding proteins involved in methymycin
       and pikromycin and desosamine biosynthesis from Streptomyces
       venezuelae
IN     Sherman, David H.; Liu, Hung-Wen; Xue, Yongquan; Zhao, Lishan
PA     Regents of the University of Minnesota, USA
SO     PCT Int. Appl., 438 pp.
```

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000000620	A2	20000106	WO 1999-US14398	19990625
WO 2000000620	A3	20000413		
US 6265202	B1	20010724	US 1998-105537	19980626
AU 9947199	A1	20000117	AU 1999-47199	19990625
EP 1090125	A2	20010411	EP 1999-930718	19990625
JP 2002536959	T2	20021105	JP 2000-557373	19990625
US 2003073824	A1	20030417	US 2001-988384	20011119
PRAI US 1998-105537	A2	19980626		
WO 1999-US14398	W	19990625		

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L9     ANSWER 15 OF 26  CAPLUS  COPYRIGHT 2004 ACS on STN
AN     1999:764178  CAPLUS
TI     Sequence and recombinant narbonolide polyketide synthase applications from
       Streptomyces venezuelae for creation of useful antibiotics
IN     Ashley, Gary; Betlach, Melanie C.; Betlach, Mary; McDaniel, Robert; Tang,
       Li
SO     PCT Int. Appl., 98 pp.
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PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9961599	A2	19991202	WO 1999-US11814	19990527
WO 9961599	A3	20000127		
US 6503741	B1	20030107	US 1998-141908	19980828
CA 2328427	AA	19991202	CA 1999-2328427	19990527
AU 9942137	A1	19991213	AU 1999-42137	19990527
AU 762399	B2	20030626		
EP 1082439	A2	20010314	EP 1999-925954	19990527FI
JP 2002516090	T2	20020604	JP 2000-550984	19990527
NZ 509006	A	20030926	NZ 1999-509006	19990527
PRAI US 1998-87080P	P	19980528		
US 1998-141908	A	19980828		
US 1998-100880P	P	19980922		
US 1999-119139P	P	19990208		
WO 1999-US11814	W	19990527		

AN   1999:548433 CAPLUS
TI   Elucidating the mechanism of chain termination switching in the
      picromycin/methymycin polyketide synthase
AU   Tang, L.; Fu, Hong; Betlach, Melanie C.; McDaniel, Robert
SO   Chemistry & Biology (1999), 6(8), 553-558

AN   1998:801708 CAPLUS
TI   Hydroxylation of macrolactones YC-17 and narbomycin is mediated
      by the pikC-encoded cytochrome P450 in Streptomyces venezuelae
AU   Xue, Yongquan; Wilson, Daniel; Zhao, Lishan; Liu, Hung-Wen; Sherman, David
      H.
SO   Chemistry & Biology (1998), 5(11), 661-667

AN   1998:679770 CAPLUS
TI   A gene cluster for macrolide antibiotic biosynthesis in
      Streptomyces venezuelae: architecture of metabolic diversity
AU   Xue, Yongquan; Zhao, Lishan; Liu, Hung-Wen; Sherman, David H.
SO   Proceedings of the National Academy of Sciences of the United States of
      America (1998), 95(21), 12111-12116

AN   1998:624768 CAPLUS
TI   Characterization of the macrolide P-450 hydroxylase from Streptomyces
      venezuelae which converts narbomycin to
      picromycin
AU   Betlach, Melanie C.; Kealey, James T.; Betlach, Mary C.; Ashley, Gary W.;
      McDaniel, Robert
SO   Biochemistry (1998), 37(42), 14937-14942

AN   1997:501482 CAPLUS
TI   Polyhydroxyalkanoate synthase recombinant production and novel pathway for
      polyhydroxyalkanoate synthesis
IN   Sherman, David H.; Williams, Mark D.; Xue, Yongquan
PA   Regents of the University of Minnesota, USA; Sherman, David H.; Williams,
      Mark D.; Xue, Yongquan
SO   PCT Int. Appl., 90 pp.

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9722711	A1	19970626	WO 1996-US20119	19961218
	EP 870053	A1	19981014	EP 1996-944849	19961218
	JP 2000502256	T2	20000229	JP 1997-522970	19961218
	US 6600029	B1	20030729	US 1998-91609	19980619
PRAI	US 1995-8847P	P	19951219		
	WO 1996-US20119	W	19961218		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2004, 23:53:32 ; Search time 10480 Seconds
                                          (without alignments)
                                          11363.351 Million cell updates/sec

Title: SEQ5-1-2911
Perfect score: 2911
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Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Database :   GenEmbl:*
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                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*

Aligned   SEQ ID NO: 30 (PikA I)
to seq ID NO: 5 (pik cluster).
Used everything 5' of the alignment
to search.
(PikA starts @ 2911 bp of SEQ:5)

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                 29:  em_vi:*
                 30:  em_htg_hum:*
                 31:  em_htg_inv:*
                 32:  em_htg_other:*
                 33:  em_htg_mus:*
                 34:  em_htg_pln:*
                 35:  em_htg_rod:*
                 36:  em_htg_mam:*
                 37:  em_htg_vrt:*
                 38:  em_sy:*
                 39:  em_htgo_hum:*
                 40:  em_htgo_mus:*
                 41:  em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2911	100.0	37948	1	AF079138	AF079138 Streptomy
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	3	405.8	13.9	834	6	AX698015	AX698015 Sequence
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c	5	346.4	11.9	36270	1	SLLINC	X79146 S.lincolnen
	6	324.2	11.1	1446	1	SLLMRBG	X62867 S.lincolnen
	7	247.8	8.5	1348	6	E07944	E07944 Mycinomycin
	8	247.8	8.5	2148	1	MPUMYRB	D14532 M.griseorub
	9	221.6	7.6	1163	1	AF462611	AF462611 Micrococc
c	10	197.4	6.8	1348	6	E07944	E07944 Mycinomycin
c	11	197.4	6.8	2148	1	MPUMYRB	D14532 M.griseorub
c	12	179.2	6.2	15100	1	AF492560	AF492560 Corynebac
c	13	178.8	6.1	834	6	AX698015	AX698015 Sequence
c	14	178.8	6.1	60196	6	AX697977	AX697977 Sequence
	15	176.6	6.1	8990	1	CXU21300	U21300 Corynebacte
c	16	176.6	6.1	51409	1	AF024666	AF024666 Corynebac
	17	176	6.0	1810	1	NG2MET	M36726 Plasmid pNG
	18	176	6.0	3123	1	AF338705	AF338705 Corynebac
	19	175	6.0	1517	1	CDERMA	X51472 Corynebacte
	20	175	6.0	4483	1	PLEMNAG	X57320 C. diphther
	21	175	6.0	4524	1	AF411029	AF411029 Propionib
	22	171.6	5.9	2198	1	AF338706	AF338706 Corynebac
	23	164.4	5.6	36270	1	SLLINC	X79146 S.lincolnen
c	24	153.8	5.3	1446	1	SLLMRBG	X62867 S.lincolnen
c	25	151.2	5.2	1430	1	SEERME1	X51891 Saccharopol
c	26	148.4	5.1	1163	1	AF462611	AF462611 Micrococc
c	27	144.4	5.0	1517	1	CDERMA	X51472 Corynebacte
c	28	144.4	5.0	2198	1	AF338706	AF338706 Corynebac
c	29	144.4	5.0	4483	1	PLEMNAG	X57320 C. diphther
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	31	143.2	4.9	15100	1	AF492560	AF492560 Corynebac
c	32	142.8	4.9	1810	1	NG2MET	M36726 Plasmid pNG
c	33	142.8	4.9	8990	1	CXU21300	U21300 Corynebacte

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2004, 22:39:56 ; Search time 739 Seconds
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Perfect score: 2911
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Scoring table: IDENTITY_NUC
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Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2911	100.0	37948	21	AAZ87285	S. venezuelae pik
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c	3	1011	34.7	1011	21	AAZ87295	S. venezuelae macr
	4	969	33.3	969	21	AAZ87296	S. venezuelae macr
c	5	360	12.4	37948	21	AAZ87285	S. venezuelae pik
	6	247.8	8.5	1348	15	AAQ67407	MyrB gene DNA, enc
c	7	197.4	6.8	1348	15	AAQ67407	MyrB gene DNA, enc
c	8	185.2	6.4	969	21	AAZ87296	S. venezuelae macr
	9	185.2	6.4	1011	21	AAZ87295	S. venezuelae macr
c	10	185.2	6.4	36778	21	AAZ87318	S. venezuelae pik
	11	134.6	4.6	114955	20	AAX53491	Human adenosine A1
c	12	132.2	4.5	1260	9	AAN81457	carB Gene sequence
c	13	129.4	4.4	114955	20	AAX53491	Human adenosine A1
	14	115	4.0	1260	9	AAN81457	carB Gene sequence
	15	86.8	3.0	154746	24	AAD25519	Human herpesvirus
c	16	86.8	3.0	154746	24	AAD25519	Human herpesvirus
	17	84.6	2.9	5760	24	ABS78661	M. echinospora DNA
c	18	82.2	2.8	3957	22	AAA09686	HSV-2 immediate ea
	19	81.8	2.8	15239	17	AAT33536	BCG deletion regio
c	20	81.8	2.8	4403765	22	AAI99683	Mycobacterium tube
c	21	81.8	2.8	4411529	22	AAI99682	Mycobacterium tube
	22	81.4	2.8	1127	21	AAA02477	Human colon cancer
	23	80.4	2.8	3957	22	AAA09686	HSV-2 immediate ea
c	24	79.6	2.7	5877	24	ABS78681	Kitasatospora sp.
	25	78.4	2.7	1459	21	AAA02528	Human colon cancer
	26	78.4	2.7	12733	24	ABK98631	Vector pEPEF14 con
	27	78.4	2.7	12739	24	ABK98592	Vector pEPEF1 cont
c	28	77	2.6	1337	20	AAZ17263	Human gene express
	29	75.8	2.6	88421	24	AAL40781	88421nt genomic DN
	30	75.6	2.6	109519	22	AAS08693	Micromonospora DNA
	31	74.2	2.5	2561	22	AAH26500	Rabbit low density
c	32	72.4	2.5	58857	21	AAA58471	Nucleotide sequenc
c	33	71.6	2.5	8438	15	AAQ73500	DNA encoding Pseud
	34	71.6	2.5	12001	16	AAQ76213	HSV L/ST region.
c	35	71.2	2.4	42999	24	ABS65032	Invertebrate forag
	36	71	2.4	712	24	ABQ40858	Oligonucleotide fo
c	37	71	2.4	712	24	ABQ40859	Oligonucleotide fo
	38	70.6	2.4	4411529	22	AAI99682	Mycobacterium tube
c	39	70.2	2.4	109519	22	AAS08693	Micromonospora DNA
c	40	70.2	2.4	125401	22	AAD17186	Streptomyces nours
c	41	69.4	2.4	2721	12	AAQ10212	BamHI J-I fragment
c	42	69.4	2.4	2721	12	AAQ10543	BamHI J-I fragment
	43	69.2	2.4	594	24	ABQ43958	Oligonucleotide fo
c	44	69.2	2.4	594	24	ABQ43959	Oligonucleotide fo
	45	69	2.4	4403765	22	AAI99683	Mycobacterium tube

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 00:31:29 ; Search time 165 Seconds
                                             (without alignments)
                                             7787.068 Million cell updates/sec

Title: SEQ5-1-2911
Perfect score: 2911
Sequence: 1 gggcccctcctcacgcgtct..........gcttccggagacggagccgg 2911

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES

                      %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   1741   59.8 36778   3   US-09-105-537-5   Sequence 5, Appli
  c 2   1011   34.7   1011   3   US-09-105-537-26   Sequence 26, Appl
     3   185.2   6.4   1011   3   US-09-105-537-26   Sequence 26, Appl
  c 4   185.2   6.4 36778   3   US-09-105-537-5   Sequence 5, Appli
     5   81.8   2.8 15239   1   US-08-390-878-17   Sequence 17, Appl
  c 6   81.8   2.8 4403765 3   US-09-103-840A-2   Sequence 2, Appli
  c 7   81.8   2.8 4411529 3   US-09-103-840A-1   Sequence 1, Appli
  c 8   71.6   2.5   8438   1   US-07-945-283-1   Sequence 1, Appli
     9   70.6   2.4 4411529 3   US-09-103-840A-1   Sequence 1, Appli
    10   70   2.4 12001   1   US-08-458-568A-11   Sequence 11, Appl
  c 11   69.4   2.4   2721   6   5215881-2   Patent No. 5215881
    12   69   2.4 4403765 3   US-09-103-840A-2   Sequence 2, Appli

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 03:12:10 ; Search time 1600 Seconds
                                         (without alignments)
                                         6412.866 Million cell updates/sec

Title: SEQ5-1-2911
Perfect score: 2911
Sequence: 1 gggcccctcctcacgcgtct..........gcttccggagacggagccgg 2911

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2911	100.0	37948	11	US-09-988-384B-5	Sequence 5, Appli
	2	1741	59.8	36778	10	US-09-861-289-5	Sequence 5, Appli
	3	1741	59.8	36778	10	US-09-860-846-5	Sequence 5, Appli
	4	1741	59.8	36778	11	US-09-836-821-5	Sequence 5, Appli
	5	1741	59.8	36778	13	US-10-271-889-48	Sequence 48, Appl
c	6	1011	34.7	1011	10	US-09-861-289-26	Sequence 26, Appl
c	7	1011	34.7	1011	10	US-09-860-846-26	Sequence 26, Appl
c	8	1011	34.7	1011	11	US-09-988-384B-26	Sequence 26, Appl
c	9	1011	34.7	1011	11	US-09-836-821-26	Sequence 26, Appl
c	10	1011	34.7	1011	13	US-10-271-889-26	Sequence 26, Appl
	11	969	33.3	969	11	US-09-988-384B-28	Sequence 28, Appl
	12	430.6	14.8	60196	15	US-10-205-032-1	Sequence 1, Appli
	13	405.8	13.9	834	15	US-10-205-032-39	Sequence 39, Appl
c	14	360	12.4	37948	11	US-09-988-384B-5	Sequence 5, Appli
c	15	185.2	6.4	969	11	US-09-988-384B-28	Sequence 28, Appl
	16	185.2	6.4	1011	10	US-09-861-289-26	Sequence 26, Appl
	17	185.2	6.4	1011	10	US-09-860-846-26	Sequence 26, Appl
	18	185.2	6.4	1011	11	US-09-988-384B-26	Sequence 26, Appl
	19	185.2	6.4	1011	11	US-09-836-821-26	Sequence 26, Appl
	20	185.2	6.4	1011	13	US-10-271-889-26	Sequence 26, Appl
c	21	185.2	6.4	36778	10	US-09-861-289-5	Sequence 5, Appli
c	22	185.2	6.4	36778	10	US-09-860-846-5	Sequence 5, Appli
c	23	185.2	6.4	36778	11	US-09-836-821-5	Sequence 5, Appli
c	24	185.2	6.4	36778	13	US-10-271-889-48	Sequence 48, Appl
c	25	178.8	6.1	834	15	US-10-205-032-39	Sequence 39, Appl
c	26	178.8	6.1	60196	15	US-10-205-032-1	Sequence 1, Appli
	27	86.8	3.0	154746	13	US-09-827-688-8	Sequence 8, Appli
c	28	86.8	3.0	154746	13	US-09-827-688-8	Sequence 8, Appli
	29	83.4	2.9	11058	15	US-10-156-761-3629	Sequence 3629, Ap
c	30	83.4	2.9	9025608	15	US-10-156-761-1	Sequence 1, Appli
c	31	82.2	2.8	3957	13	US-10-200-562-193	Sequence 193, App
c	32	82.2	2.8	3957	13	US-10-237-551-193	Sequence 193, App
	33	80.4	2.8	3957	13	US-10-200-562-193	Sequence 193, App
	34	80.4	2.8	3957	13	US-10-237-551-193	Sequence 193, App
	35	78.6	2.7	5355	15	US-10-205-032-19	Sequence 19, Appl
	36	78.4	2.7	12733	15	US-10-032-393-47	Sequence 47, Appl
	37	78.4	2.7	12739	15	US-10-032-393-8	Sequence 8, Appli
	38	76.6	2.6	3133	12	US-10-292-798-1191	Sequence 1191, Ap
	39	76.6	2.6	3133	13	US-10-017-161-1483	Sequence 1483, Ap
	40	75.8	2.6	88421	10	US-09-976-059-1	Sequence 1, Appli
	41	75.2	2.6	1413	15	US-10-156-761-5135	Sequence 5135, Ap
	42	75.2	2.6	9025608	15	US-10-156-761-1	Sequence 1, Appli
c	43	74.4	2.6	15738	13	US-10-329-079-46	Sequence 46, Appl
c	44	74.4	2.6	61944	13	US-10-329-079-34	Sequence 34, Appl
	45	74.2	2.5	2561	10	US-09-976-740-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-09-988-384B-5

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 00:17:17 ; Search time 5853 Seconds
                                               (without alignments)
                                               12087.875 Million cell updates/sec

Title: SEQ5-1-2911
Perfect score: 2911
Sequence: 1 gggcccctcctcacgcgtct..........gcttccggagacggagccgg 2911

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                   1:   em_estba:*
                   2:   em_esthum:*
                   3:   em_estin:*
                   4:   em_estmu:*
                   5:   em_estov:*
                   6:   em_estpl:*
                   7:   em_estro:*
                   8:   em_htc:*
                   9:   gb_est1:*
                   10: gb_est2:*
                   11: gb_htc:*
                   12: gb_est3:*
                   13: gb_est4:*
                   14: gb_est5:*
                   15: em_estfun:*
                   16: em_estom:*
                   17: em_gss_hum:*
                   18: em_gss_inv:*
                   19: em_gss_pln:*
                   20: em_gss_vrt:*
                   21: em_gss_fun:*
                   22: em_gss_mam:*
                   23: em_gss_mus:*
                   24: em_gss_pro:*
                   25: em_gss_rod:*
                   26: em_gss_phg:*
                   27: em_gss_vrl:*
                   28: gb_gss1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	133.6	4.6	1309	29	AG077201	AG077201 Pan trogl
c	2	132.8	4.6	1159	29	CC210735	CC210735 CH261-185
c	3	131.6	4.5	1695	29	CC290874	CC290874 CH261-172
c	4	122.8	4.2	1281	12	BG852363	BG852363 1024034A0
c	5	120.6	4.1	1198	29	CC190008	CC190008 CH261-138
c	6	120.6	4.1	1785	29	CC219595	CC219595 CH261-62D
c	7	118	4.1	1516	12	BG809984	BG809984 mgct002xd
	8	117	4.0	1798	29	AG171124	AG171124 Pan trogl
c	9	116.4	4.0	1798	29	AG171124	AG171124 Pan trogl
c	10	116	4.0	1610	29	BZ569386	BZ569386 pacs2-164
c	11	114.6	3.9	1242	12	BM911414	BM911414 AGENCOURT
	12	114.6	3.9	1299	29	AG039481	AG039481 Pan trogl
c	13	114.2	3.9	1121	29	AG062320	AG062320 Pan trogl
	14	113.8	3.9	1016	29	CNS03LU9	AL249930 Tetraodon
c	15	112	3.8	1250	29	AG043469	AG043469 Pan trogl
c	16	111.4	3.8	1288	13	BQ678719	BQ678719 AGENCOURT
	17	111.4	3.8	1651	12	BG809816	BG809816 mgct001xk
	18	110.8	3.8	1169	29	AG032383	AG032383 Pan trogl
c	19	110.4	3.8	1598	29	AG030579	AG030579 Pan trogl
	20	110.2	3.8	1474	29	BZ569821	BZ569821 msh2_1034
c	21	109.6	3.8	1122	29	CC231036	CC231036 CH261-27F
	22	109	3.7	1341	29	AG030611	AG030611 Pan trogl
	23	108.8	3.7	1170	29	AG111669	AG111669 Pan trogl
	24	108.4	3.7	1137	12	BG809979	BG809979 mgct002xd
	25	108.2	3.7	1516	12	BG809984	BG809984 mgct002xd
	26	108	3.7	947	29	AG069825	AG069825 Pan trogl
	27	108	3.7	1052	13	BX354803	BX354803 BX354803
c	28	107.6	3.7	1767	29	CC294031	CC294031 CH261-82A
c	29	107.4	3.7	1116	29	BZ569478	BZ569478 pacs2-164
	30	107	3.7	1321	29	AG126084	AG126084 Pan trogl
	31	106.8	3.7	1121	29	AG062320	AG062320 Pan trogl
	32	106.8	3.7	1160	29	AG043473	AG043473 Pan trogl
	33	106.6	3.7	1116	29	BZ569478	BZ569478 pacs2-164
	34	106.4	3.7	1364	12	BM810045	BM810045 AGENCOURT
c	35	106.4	3.7	1538	29	AG030607	AG030607 Pan trogl
	36	106.4	3.7	1625	29	AG043477	AG043477 Pan trogl
	37	106.2	3.6	1126	29	AG064051	AG064051 Pan trogl
	38	106	3.6	1448	29	CC220110	CC220110 CH261-92F
c	39	105.6	3.6	1136	29	CC292742	CC292742 CH261-185
c	40	105.4	3.6	1700	29	CC298790	CC298790 CH261-106
c	41	105.2	3.6	1370	29	AG072551	AG072551 Pan trogl
	42	105.2	3.6	1538	29	AG030607	AG030607 Pan trogl
	43	104.8	3.6	1369	29	AG081191	AG081191 Pan trogl
c	44	104.4	3.6	1026	29	BZ569417	BZ569417 pacs2-164
	45	104.4	3.6	1309	29	AG077201	AG077201 Pan trogl

WEST Search History

| Hide Items | Restore | Clear | Cancel |

DATE: Tuesday, January 13, 2004

Hide?	Set Name	Query	Hit Count
		DB=USPT; PLUR=YES; OP=OR	
☐	L7	L6 same (polyketide adj synthase)	14
☐	L6	l3 or picromycin	138
☐	L5	L4 and (polyketide adj synthase)	23
☐	L4	L3 and venezuelae	60
☐	L3	$methymycin or pikromycin or narbomycin	121
☐	L2	6503741.pn.	1
☐	L1	6265202.pn.	1

END OF SEARCH HISTORY